

Emilio O Casamayor

List of Publications by Year in descending order

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Version: 2024-02-01

138
papers

12,307
citations

30070

54
h-index

27406

106
g-index

143
all docs

143
docs citations

143
times ranked

12577
citing authors

#	ARTICLE	IF	CITATIONS
1	Using network analysis to explore co-occurrence patterns in soil microbial communities. ISME Journal, 2012, 6, 343-351.	9.8	2,051
2	Ecology of the rare microbial biosphere of the Arctic Ocean. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22427-22432.	7.1	488
3	Changes in archaeal, bacterial and eukaryal assemblages along a salinity gradient by comparison of genetic fingerprinting methods in a multipond solar saltern. Environmental Microbiology, 2002, 4, 338-348.	3.8	433
4	Global ecological patterns in uncultured Archaea. ISME Journal, 2010, 4, 182-190.	9.8	406
5	Microbial Ecology of an Extreme Acidic Environment, the Tinto River. Applied and Environmental Microbiology, 2003, 69, 4853-4865.	3.1	403
6	Bacterial Community Structure Associated with a Dimethylsulfoniopropionate-Producing North Atlantic Algal Bloom. Applied and Environmental Microbiology, 2000, 66, 4237-4246.	3.1	402
7	Identification of and Spatio-Temporal Differences between Microbial Assemblages from Two Neighboring Sulfurous Lakes: Comparison by Microscopy and Denaturing Gradient Gel Electrophoresis. Applied and Environmental Microbiology, 2000, 66, 499-508.	3.1	392
8	Prokaryotic genetic diversity throughout the salinity gradient of a coastal solar saltern. Environmental Microbiology, 2002, 4, 349-360.	3.8	287
9	Differential photoinhibition of bacterial and archaeal ammonia oxidation. FEMS Microbiology Letters, 2012, 327, 41-46.	1.8	245
10	DOES ECOSYSTEM SIZE DETERMINE AQUATIC BACTERIAL RICHNESS?. Ecology, 2005, 86, 1715-1722.	3.2	238
11	Dynamics of bacterial community succession in a salt marsh chronosequence: evidences for temporal niche partitioning. ISME Journal, 2014, 8, 1989-2001.	9.8	221
12	Global phylogenetic community structure and β -diversity patterns in surface bacterioplankton metacommunities. Aquatic Microbial Ecology, 2010, 59, 1-10.	1.8	195
13	Hydrography shapes bacterial biogeography of the deep Arctic Ocean. ISME Journal, 2010, 4, 564-576.	9.8	179
14	Distribution of prokaryotic genetic diversity in athalassohaline lakes of the Atacama Desert, Northern Chile. FEMS Microbiology Ecology, 2004, 48, 57-69.	2.7	163
15	Unique archaeal assemblages in the Arctic Ocean unveiled by massively parallel tag sequencing. ISME Journal, 2009, 3, 860-869.	9.8	163
16	Changes in marine bacterioplankton phylogenetic composition during incubations designed to measure biogeochemically significant parameters. Limnology and Oceanography, 2001, 46, 1181-1188.	3.1	162
17	A long-term survey unveils strong seasonal patterns in the airborne microbiome coupled to general and regional atmospheric circulations. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12229-12234.	7.1	161
18	Viability and potential for immigration of airborne bacteria from Africa that reach high mountain lakes in Europe. Environmental Microbiology, 2009, 11, 1612-1623.	3.8	141

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19	Molecular characterization of microbial populations in a low-grade copper ore bioleaching test heap. <i>Hydrometallurgy</i> , 2005, 80, 241-253.	4.3	134
20	A survey on bacteria inhabiting the sea surface microlayer of coastal ecosystems. <i>FEMS Microbiology Ecology</i> , 2005, 54, 269-280.	2.7	133
21	Interannual recurrence of archaeal assemblages in the coastal NW Mediterranean Sea (Blanes Bay) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i>	3.1	131
22	High bicarbonate assimilation in the dark by Arctic bacteria. <i>ISME Journal</i> , 2010, 4, 1581-1590.	9.8	131
23	Microheterogeneity in 16S Ribosomal DNA-Defined Bacterial Populations from a Stratified Planktonic Environment Is Related to Temporal Changes and to Ecological Adaptations. <i>Applied and Environmental Microbiology</i> , 2002, 68, 1706-1714.	3.1	124
24	Connecting biodiversity and potential functional role in modern euxinic environments by microbial metagenomics. <i>ISME Journal</i> , 2015, 9, 1648-1661.	9.8	123
25	Novelty and spatio-temporal heterogeneity in the bacterial diversity of hypersaline Lake Tebenquiche (Salar de Atacama). <i>Extremophiles</i> , 2008, 12, 491-504.	2.3	118
26	Consistent changes in the taxonomic structure and functional attributes of bacterial communities during primary succession. <i>ISME Journal</i> , 2018, 12, 1658-1667.	9.8	113
27	High occurrence of <i>Pacearchaeota</i> and <i>Woesearchaeota</i> (<i>Archaea</i>) <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10</i> <i>Environmental Microbiology Reports</i> , 2016, 8, 210-217.	2.4	112
28	Effect of Saharan dust inputs on bacterial activity and community composition in Mediterranean lakes and reservoirs. <i>Limnology and Oceanography</i> , 2009, 54, 869-879.	3.1	111
29	The microbial contribution to macroecology. <i>Frontiers in Microbiology</i> , 2014, 5, 203.	3.5	106
30	Vertical segregation and phylogenetic characterization of ammonia-oxidizing Archaea in a deep oligotrophic lake. <i>ISME Journal</i> , 2012, 6, 1786-1797.	9.8	105
31	A transplant experiment to identify the factors controlling bacterial abundance, activity, production, and community composition in a eutrophic canyon-shaped reservoir. <i>Limnology and Oceanography</i> , 2002, 47, 62-77.	3.1	104
32	Comparison of samplers for the biological characterization of the sea surface microlayer. <i>Limnology and Oceanography: Methods</i> , 2004, 2, 213-225.	2.0	101
33	Insights in the ecology and evolutionary history of the <i>Miscellaneous Crenarchaeotic Group</i> lineage. <i>ISME Journal</i> , 2016, 10, 665-677.	9.8	100
34	Diversity of planktonic photoautotrophic microorganisms along a salinity gradient as depicted by microscopy, flow cytometry, pigment analysis and DNA-based methods. <i>FEMS Microbiology Ecology</i> , 2004, 49, 281-293.	2.7	98
35	Seasonal Changes of Freshwater Ammonia-Oxidizing Archaeal Assemblages and Nitrogen Species in Oligotrophic Alpine Lakes. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1937-1945.	3.1	98
36	A hotspot for cold crenarchaeota in the neuston of high mountain lakes. <i>Environmental Microbiology</i> , 2008, 10, 1080-1086.	3.8	97

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37	Distribution of Microbial Arsenic Reduction, Oxidation and Extrusion Genes along a Wide Range of Environmental Arsenic Concentrations. PLoS ONE, 2013, 8, e78890.	2.5	97
38	Structure, inter-annual recurrence, and global-scale connectivity of airborne microbial communities. Science of the Total Environment, 2014, 487, 187-195.	8.0	89
39	Bacterial "cosmopolitanism"™ and importance of local environmental factors for community composition in remote high-altitude lakes. Freshwater Biology, 2009, 54, 994-1005.	2.4	88
40	Experimental test of bacteria-phytoplankton coupling in the Southern Ocean. Limnology and Oceanography, 2005, 50, 1844-1854.	3.1	85
41	Patterns and architecture of genomic islands in marine bacteria. BMC Genomics, 2012, 13, 347.	2.8	84
42	Exploration of community traits as ecological markers in microbial metagenomes. Molecular Ecology, 2012, 21, 1909-1917.	3.9	84
43	Showcasing the role of seawater in bacteria recruitment and microbiome stability in sponges. Scientific Reports, 2018, 8, 15201.	3.3	82
44	High archaeal richness in the water column of a freshwater sulfurous karstic lake along an interannual study. FEMS Microbiology Ecology, 2008, 66, 331-342.	2.7	81
45	Vertical Distribution of Ammonia-Oxidizing Crenarchaeota and Methanogens in the Epipelagic Waters of Lake Kivu (Rwanda-Democratic Republic of the Congo). Applied and Environmental Microbiology, 2010, 76, 6853-6863.	3.1	81
46	Genetic diversity of planktonic eukaryotes in high mountain lakes (Central Pyrenees, Spain). Environmental Microbiology, 2012, 14, 2445-2456.	3.8	81
47	Degradation of sulfonamides as a microbial resistance mechanism. Water Research, 2017, 115, 309-317.	11.3	81
48	Regional and global elevational patterns of microbial species richness and evenness. Ecography, 2017, 40, 393-402.	4.5	79
49	High similarity between bacterioneuston and airborne bacterial community compositions in a high mountain lake area. FEMS Microbiology Ecology, 2009, 67, 219-228.	2.7	75
50	Microbial biodiversity in saline shallow lakes of the Monegros Desert, Spain. FEMS Microbiology Ecology, 2013, 85, 503-518.	2.7	72
51	Partitioning of <i>Thaumarchaeota</i> populations along environmental gradients in high mountain lakes. FEMS Microbiology Ecology, 2013, 84, 154-164.	2.7	71
52	Macrophyte landscape modulates lake ecosystem-level nitrogen losses through tightly coupled plant-microbe interactions. Limnology and Oceanography, 2016, 61, 78-88.	3.1	71
53	Stream Hydrological Fragmentation Drives Bacterioplankton Community Composition. PLoS ONE, 2013, 8, e64109.	2.5	58
54	Carbon dioxide fixation in the dark by photosynthetic bacteria in sulfide-rich stratified lakes with oxic-anoxic interfaces. Limnology and Oceanography, 2008, 53, 1193-1203.	3.1	57

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55	Habitat-Associated Phylogenetic Community Patterns of Microbial Ammonia Oxidizers. PLoS ONE, 2012, 7, e47330.	2.5	55
56	Exploring the Links between Natural Products and Bacterial Assemblages in the Sponge <i>Aplysina aerophoba</i> . Applied and Environmental Microbiology, 2011, 77, 862-870.	3.1	54
57	High planktonic diversity in mountain lakes contains similar contributions of autotrophic, heterotrophic and parasitic eukaryotic life forms. Scientific Reports, 2018, 8, 4457.	3.3	51
58	Sponges and Their Microbiomes Show Similar Community Metrics Across Impacted and Well-Preserved Reefs. Frontiers in Microbiology, 2019, 10, 1961.	3.5	49
59	Euxinic Freshwater Hypolimnia Promote Bacterial Endemicity in Continental Areas. Microbial Ecology, 2011, 61, 465-472.	2.8	46
60	High-diversity biofilm for the oxidation of sulfide-containing effluents. Applied Microbiology and Biotechnology, 2004, 64, 726-734.	3.6	45
61	ENDOSYMBIOTIC CALCIFYING BACTERIA: A NEW CUE TO THE ORIGIN OF CALCIFICATION IN METAZOA?. Evolution; International Journal of Organic Evolution, 2012, 66, 2993-2999.	2.3	45
62	Bioaerosols in the Barcelona subway system. Indoor Air, 2017, 27, 564-575.	4.3	45
63	Wastewater Treatment Plant Effluents Change Abundance and Composition of Ammonia-Oxidizing Microorganisms in Mediterranean Urban Stream Biofilms. Microbial Ecology, 2015, 69, 66-74.	2.8	44
64	The DNRA-Denitrification Dichotomy Differentiates Nitrogen Transformation Pathways in Mountain Lake Benthic Habitats. Frontiers in Microbiology, 2019, 10, 1229.	3.5	44
65	Influence of Edaphic, Climatic, and Agronomic Factors on the Composition and Abundance of Nitrifying Microorganisms in the Rhizosphere of Commercial Olive Crops. PLoS ONE, 2015, 10, e0125787.	2.5	44
66	Microbial ecology of the atmosphere. FEMS Microbiology Reviews, 2022, 46, .	8.6	44
67	High Bacterial Diversity in Epilithic Biofilms of Oligotrophic Mountain Lakes. Microbial Ecology, 2012, 64, 860-869.	2.8	41
68	Diel gene expression profiles of a phosphorus limited mountain lake using metatranscriptomics. Environmental Microbiology, 2013, 15, 1190-1203.	3.8	41
69	Unifying the known and unknown microbial coding sequence space. ELife, 2022, 11, .	6.0	41
70	Contribution of deep dark fixation processes to overall CO ₂ incorporation and large vertical changes of microbial populations in stratified karstic lakes. Aquatic Sciences, 2012, 74, 61-75.	1.5	40
71	The dominant detritus-feeding invertebrate in Arctic peat soils derives its essential amino acids from gut symbionts. Journal of Animal Ecology, 2016, 85, 1275-1285.	2.8	40
72	Speciation and ecological success in dimly lit waters: horizontal gene transfer in a green sulfur bacteria bloom unveiled by metagenomic assembly. ISME Journal, 2017, 11, 201-211.	9.8	40

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73	5S rRNA fingerprints of marine bacteria, halophilic archaea and natural prokaryotic assemblages along a salinity gradient. <i>FEMS Microbiology Ecology</i> , 2000, 34, 113-119.	2.7	39
74	Flow cytometric identification and enumeration of photosynthetic sulfur bacteria and potential for ecophysiological studies at the single-cell level. <i>Environmental Microbiology</i> , 2007, 9, 1969-1985.	3.8	38
75	Phylogenetic ecology of widespread uncultured clades of the Kingdom Euryarchaeota. <i>Molecular Ecology</i> , 2011, 20, 1988-1996.	3.9	36
76	High genetic diversity and novelty in planktonic protists inhabiting inland and coastal high salinity water bodies. <i>FEMS Microbiology Ecology</i> , 2013, 85, 27-36.	2.7	36
77	Bacterial and archaeal community structure in the surface microlayer of high mountain lakes examined under two atmospheric aerosol loading scenarios. <i>FEMS Microbiology Ecology</i> , 2013, 84, 387-397.	2.7	36
78	Nitrogen-Cycling Genes in Epilithic Biofilms of Oligotrophic High-Altitude Lakes (Central Pyrenees.) <i>Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50</i>	2.8	35
79	Stream drying drives microbial ammonia oxidation and first-flush nitrate export. <i>Ecology</i> , 2016, 97, 2192-2198.	3.2	35
80	Environmental controls and composition of anoxygenic photoheterotrophs in ultraoligotrophic high-altitude lakes (Central Pyrenees). <i>Environmental Microbiology Reports</i> , 2014, 6, 145-151.	2.4	33
81	Partitioning of CO ₂ Incorporation Among Planktonic Microbial Guilds and Estimation of In Situ Specific Growth Rates. <i>Microbial Ecology</i> , 2005, 50, 230-241.	2.8	32
82	Biofilm recovery in a wastewater treatment plant-influenced stream and spatial segregation of ammonia-oxidizing microbial populations. <i>Limnology and Oceanography</i> , 2011, 56, 1054-1064.	3.1	32
83	A close link between bacterial community composition and environmental heterogeneity in maritime Antarctic lakes. <i>International Microbiology</i> , 2010, 13, 67-77.	2.4	32
84	Fingerprinting the genetic diversity of the biotin carboxylase gene (<i>accC</i>) in aquatic ecosystems as a potential marker for studies of carbon dioxide assimilation in the dark. <i>Environmental Microbiology</i> , 2008, 10, 2527-2536.	3.8	31
85	Active bacteria and archaea cells fixing bicarbonate in the dark along the water column of a stratified eutrophic lagoon. <i>FEMS Microbiology Ecology</i> , 2011, 77, 370-384.	2.7	31
86	Primary production in estuarine oxic/anoxic interfaces: contribution of microbial dark CO ₂ fixation in the Ebro River Salt Wedge Estuary. <i>Marine Ecology - Progress Series</i> , 2001, 215, 49-56.	1.9	31
87	Temperature drives local contributions to beta diversity in mountain streams: Stochastic and deterministic processes. <i>Global Ecology and Biogeography</i> , 2020, 29, 420-432.	5.8	30
88	Microbial food web components, bulk metabolism, and single-cell physiology of piconeuston in surface microlayers of high-altitude lakes. <i>Frontiers in Microbiology</i> , 2015, 6, 361.	3.5	29
89	High similarity in bacterial bioaerosol compositions between the free troposphere and atmospheric depositions collected at high-elevation mountains. <i>Atmospheric Environment</i> , 2019, 203, 79-86.	4.1	28
90	Climate mediates continental scale patterns of stream microbial functional diversity. <i>Microbiome</i> , 2020, 8, 92.	11.1	28

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91	Spatial comparison of total vs. active bacterial populations by coupling genetic fingerprinting and clone library analyses in the NW Mediterranean Sea. <i>FEMS Microbiology Ecology</i> , 2009, 67, 30-42.	2.7	27
92	Catalyzed Reported Deposition-Fluorescence In Situ Hybridization Protocol To Evaluate Phagotrophy in Mixotrophic Protists. <i>Applied and Environmental Microbiology</i> , 2005, 71, 7321-7326.	3.1	25
93	Targeting spatiotemporal dynamics of planktonic ammonia-oxidizing thaumarchaeota ecotypes by newly designed primers and quantitative polymerase chain reaction. <i>Environmental Microbiology</i> , 2014, 16, 689-700.	3.8	25
94	Vertically aligned carbon nanotubes coated with manganese dioxide as cathode material for microbial fuel cells. <i>Journal of Materials Science</i> , 2015, 50, 1214-1220.	3.7	25
95	Potential Effect of Freshwater Virus on the Structure and Activity of Bacterial Communities in the Marennes-Oléron Bay (France). <i>Microbial Ecology</i> , 2009, 57, 295-306.	2.8	24
96	A close relationship between primary nucleotides sequence structure and the composition of functional genes in the genome of prokaryotes. <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 650-658.	2.7	22
97	The phylogenetic and ecological context of cultured and whole genome-sequenced planktonic bacteria from the coastal NW Mediterranean Sea. <i>Systematic and Applied Microbiology</i> , 2014, 37, 216-228.	2.8	22
98	Regional community assembly drivers and microbial environmental sources shaping bacterioplankton in an alpine lacustrine district (Pyrenees, Spain). <i>Environmental Microbiology</i> , 2020, 22, 297-309.	3.8	22
99	Photoinhibition on natural ammonia oxidizers biofilm populations and implications for nitrogen uptake in stream biofilms. <i>Limnology and Oceanography</i> , 2017, 62, 364-375.	3.1	21
100	A phylogenetic perspective on species diversity, β -diversity and biogeography for the microbial world. <i>Molecular Ecology</i> , 2014, 23, 5868-5876.	3.9	20
101	Partitioning between atmospheric deposition and canopy microbial nitrification into throughfall nitrate fluxes in a Mediterranean forest. <i>Journal of Ecology</i> , 2020, 108, 626-640.	4.0	20
102	Different Marine Heterotrophic Nanoflagellates Affect Differentially the Composition of Enriched Bacterial Communities. <i>Microbial Ecology</i> , 2005, 49, 474-485.	2.8	19
103	Taxonomy and functional interactions in upper and bottom waters of an oligotrophic high-mountain deep lake (Redon, Pyrenees) unveiled by microbial metagenomics. <i>Science of the Total Environment</i> , 2020, 707, 135929.	8.0	19
104	Heterogeneous vertical structure of the bacterioplankton community in a non-stratified Antarctic lake. <i>Antarctic Science</i> , 2013, 25, 229-238.	0.9	18
105	High Bacterial Diversity and Phylogenetic Novelty in Dark Euxinic Freshwaters Analyzed by 16S Tag Community Profiling. <i>Microbial Ecology</i> , 2016, 71, 566-574.	2.8	18
106	Microbial composition, potential functional roles and genetic novelty in gypsum-rich and hypersaline soils of Monegros and Gallocanta (Spain). <i>Science of the Total Environment</i> , 2019, 650, 343-353.	8.0	18
107	Ecological and Metabolic Thresholds in the Bacterial, Protist, and Fungal Microbiome of Ephemeral Saline Lakes (Monegros Desert, Spain). <i>Microbial Ecology</i> , 2021, 82, 885-896.	2.8	18
108	Vertical distribution of planktonic autotrophic thiobacilli and dark CO ₂ fixation rates in lakes with oxygen-sulfide interfaces. <i>Aquatic Microbial Ecology</i> , 2010, 59, 217-228.	1.8	18

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109	Comparison of pure cultures and natural assemblages of planktonic photosynthetic sulfur bacteria by low molecular mass RNA fingerprinting. <i>FEMS Microbiology Ecology</i> , 2000, 32, 25-34.	2.7	17
110	Comparison of <i>Artemia</i> bacteria associations in brines, laboratory cultures and the gut environment: a study based on Chilean hypersaline environments. <i>Extremophiles</i> , 2015, 19, 135-147.	2.3	17
111	A Randomized Trait Community Clustering approach to unveil consistent environmental thresholds in community assembly. <i>ISME Journal</i> , 2019, 13, 2681-2689.	9.8	17
112	Microbial Community Structure and Functionality in the Deep Sea Floor: Evaluating the Causes of Spatial Heterogeneity in a Submarine Canyon System (NW Mediterranean, Spain). <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	17
113	Winter to spring changes in the slush bacterial community composition of a high mountain lake (Lake Tj ETQq1 1 0,784314 rgBT /Ov	2.4	15
114	Contrasting activity patterns determined by BrdU incorporation in bacterial ribotypes from the Arctic Ocean in winter. <i>Frontiers in Microbiology</i> , 2013, 4, 118.	3.5	14
115	Identification of phototrophic sulfur bacteria through the analysis of 16S rRNA band patterns. <i>Archives of Microbiology</i> , 1998, 170, 269-278.	2.2	13
116	In Situ Assessment on the Physiological State of Purple and Green Sulfur Bacteria through the Analyses of Pigment and 5S rRNA Content. <i>Microbial Ecology</i> , 2001, 42, 427-437.	2.8	13
117	High protists diversity in the plankton of sulfurous lakes and lagoons examined by 18S rRNA gene sequence analyses. <i>Environmental Microbiology Reports</i> , 2015, 7, 908-917.	2.4	12
118	Colonization and extinction rates estimated from temporal dynamics of ecological communities: The island r package. <i>Methods in Ecology and Evolution</i> , 2019, 10, 1108-1117.	5.2	12
119	Individual fate and gut microbiome composition in the European wild rabbit (<i>Oryctolagus cuniculus</i>). <i>Scientific Reports</i> , 2021, 11, 766.	3.3	12
120	The characteristic time of ecological communities. <i>Ecology</i> , 2021, 102, e03247.	3.2	11
121	Dynamics and ecological distributions of the Archaea microbiome from inland saline lakes (Monegros) Tj ETQq1 1 0,784314 rgBT /Ov	2.7	11
122	Environmental distribution of two widespread uncultured freshwater <i>Euryarchaeota</i> clades unveiled by specific primers and quantitative PCR. <i>Environmental Microbiology Reports</i> , 2013, 5, 861-867.	2.4	10
123	Towards a Microbial Conservation Perspective in High Mountain Lakes. <i>Advances in Global Change Research</i> , 2017, , 157-180.	1.6	10
124	Ecophysiological significance of scale-dependent patterns in prokaryotic genomes unveiled by a combination of statistic and genometric analyses. <i>Genomics</i> , 2008, 91, 538-543.	2.9	9
125	A long-term atmospheric baseline for intercontinental exchange of airborne pathogens. <i>Environment International</i> , 2022, 158, 106916.	10.0	9
126	T-RFPred: a nucleotide sequence size prediction tool for microbial community description based on terminal-restriction fragment length polymorphism chromatograms. <i>BMC Microbiology</i> , 2010, 10, 262.	3.3	8

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127	DOES ECOSYSTEM SIZE DETERMINE AQUATIC BACTERIA RICHNESS? REPLY. <i>Ecology</i> , 2007, 88, 253-255.	3.2	8
128	General decline in the diversity of the airborne microbiota under future climatic scenarios. <i>Scientific Reports</i> , 2021, 11, 20223.	3.3	8
129	Global dispersal and potential sources of antibiotic resistance genes in atmospheric remote depositions. <i>Environment International</i> , 2022, 160, 107077.	10.0	8
130	Maintenance of previously uncultured freshwater archaea from anoxic waters under laboratory conditions. <i>Antonie Van Leeuwenhoek</i> , 2011, 99, 403-408.	1.7	6
131	Environmental Heterogeneity and Microbial Inheritance Influence Sponge-Associated Bacterial Composition of <i>Spongia lamella</i> . <i>Microbial Ecology</i> , 2014, 68, 611-620.	2.8	5
132	Dayâ€night ammonium oxidation in an urban stream: the influence of irradiance on ammonia oxidizers. <i>Freshwater Science</i> , 2017, 36, 272-283.	1.8	4
133	Development of a 16S rRNA-targeted fluorescence in situ hybridization probe for quantification of the ammonia-oxidizer <i>Nitrosotalea devanattera</i> and its relatives. <i>Systematic and Applied Microbiology</i> , 2018, 41, 408-413.	2.8	3
134	5S rRNA fingerprints of marine bacteria, halophilic archaea and natural prokaryotic assemblages along a salinity gradient. <i>FEMS Microbiology Ecology</i> , 2000, 34, 113-119.	2.7	3
135	Sodium Dodecyl Sulfate-Polyacrylamide Gel Protein Electrophoresis of Freshwater Photosynthetic Sulfur Bacteria. <i>Current Microbiology</i> , 2011, 62, 111-116.	2.2	2
136	Biological Microbial Interactions from Cooccurrence Networks in a High Mountain Lacustrine District. <i>MSphere</i> , 2022, 7, .	2.9	1
137	Comparison of pure cultures and natural assemblages of planktonic photosynthetic sulfur bacteria by low molecular mass RNA fingerprinting. <i>FEMS Microbiology Ecology</i> , 2000, 32, 25-34.	2.7	0
138	Microbial metabolic routes in metagenome assembled genomes are mirrored by the mass balance of polycyclic aromatic hydrocarbons in a high altitude lake. <i>Environmental Pollution</i> , 2022, 308, 119592.	7.5	0